

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/444,994DATE: 11/21/95
TIME: 08:56:55

INPUT SET: S7400.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Palese, Peter
O'Neill, Robert(ii) TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL
COMPOUNDS THAT INHIBIT INTERACTION OF HOST CELL PROTEINS
AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/444,994
(B) FILING DATE: 19-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 6923-054

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-9741/8864
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 19 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51

52 (ii) MOLECULE TYPE: DNA
53
54
55
56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58

59 GCAAAGCAGG AGAAACCAC
60

19

61 (2) INFORMATION FOR SEQ ID NO:2:
62

63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 24 base pairs
65 (B) TYPE: nucleic acid
66 (C) STRANDEDNESS: single
67 (D) TOPOLOGY: linear
68

69 (ii) MOLECULE TYPE: DNA
70
71
72
73

74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
75

76 GGGTCCATCT GATAGATATG AGAG
77

24

78 (2) INFORMATION FOR SEQ ID NO:3:
79

80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 48 base pairs
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: single
84 (D) TOPOLOGY: linear
85

86 (ii) MOLECULE TYPE: DNA
87
88

89 (ix) FEATURE:

90 (A) NAME/KEY: modified_base
91 (B) LOCATION: 36
92 (D) OTHER INFORMATION: /mod_base= i
93

94 (ix) FEATURE:

95 (A) NAME/KEY: modified_base
96 (B) LOCATION: 37
97 (D) OTHER INFORMATION: /mod_base= i
98

99 (ix) FEATURE:

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100 (A) NAME/KEY: modified_base
101 (B) LOCATION: 41
102 (D) OTHER INFORMATION: /mod_base= i
103
104 (ix) FEATURE:
105 (A) NAME/KEY: modified_base
106 (B) LOCATION: 42
107 (D) OTHER INFORMATION: /mod_base= i
108
109 (ix) FEATURE:
110 (A) NAME/KEY: modified_base
111 (B) LOCATION: 46
112 (D) OTHER INFORMATION: /mod_base= i
113
114 (ix) FEATURE:
115 (A) NAME/KEY: modified_base
116 (B) LOCATION: 47
117 (D) OTHER INFORMATION: /mod_base= i
118
119
120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
121
122 CUACUACUAC UAGGCCACGC GTCGACTACT ACGGGNNGG NNGGGNNG
123
124 (2) INFORMATION FOR SEQ ID NO:4:
125
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 20 base pairs
128 (B) TYPE: nucleic acid
129 (C) STRANDEDNESS: single
130 (D) TOPOLOGY: linear
131
132 (ii) MOLECULE TYPE: DNA
133
134
135
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
138
139 TCCTGATGTT GCTGTAGACG
140
141 (2) INFORMATION FOR SEQ ID NO:5:
142
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH: 20 base pairs
145 (B) TYPE: nucleic acid
146 (C) STRANDEDNESS: single
147 (D) TOPOLOGY: linear
148
149 (ii) MOLECULE TYPE: DNA
150
151
152

48

20

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153
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
155

156 GCACGACTAG TATGATTGTC
157

20

158 (2) INFORMATION FOR SEQ ID NO:6:
159

160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 8 amino acids
162 (B) TYPE: amino acid
163 (C) STRANDEDNESS:
164 (D) TOPOLOGY: unknown
165

166 (ii) MOLECULE TYPE: peptide
167
168
169
170

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

172
173 Thr Gly Ala Gly Ala Gly Leu Gly
174 1 5
175

176 (2) INFORMATION FOR SEQ ID NO:7:
177

178 (i) SEQUENCE CHARACTERISTICS:
179 (A) LENGTH: 5 amino acids
180 (B) TYPE: amino acid
181 (C) STRANDEDNESS:
182 (D) TOPOLOGY: unknown
183

184 (ii) MOLECULE TYPE: peptide
185
186
187
188

189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

190
191 Tyr Ser Ala Ala Lys
192 1 5
193

194 (2) INFORMATION FOR SEQ ID NO:8:
195

196 (i) SEQUENCE CHARACTERISTICS:
197 (A) LENGTH: 27 base pairs
198 (B) TYPE: nucleic acid
199 (C) STRANDEDNESS: single
200 (D) TOPOLOGY: unknown
201

202 (ii) MOLECULE TYPE: DNA
203
204

205 (ix) FEATURE:

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206 (A) NAME/KEY: CDS
207 (B) LOCATION: 1..27
208
209
210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
211
212 GAC TGG CTG GAA TTC CCC ATG GCG TCC 27
213 Asp Trp Leu Glu Phe Pro Met Ala Ser
214 1 5
215
216
217 (2) INFORMATION FOR SEQ ID NO:9:
218
219 (i) SEQUENCE CHARACTERISTICS:
220 (A) LENGTH: 9 amino acids
221 (B) TYPE: amino acid
222 (D) TOPOLOGY: linear
223
224 (ii) MOLECULE TYPE: protein
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
227
228 Asp Trp Leu Glu Phe Pro Met Ala Ser
229 1 5
230
231 (2) INFORMATION FOR SEQ ID NO:10:
232
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 2940 base pairs
235 (B) TYPE: nucleic acid
236 (C) STRANDEDNESS: unknown
237 (D) TOPOLOGY: unknown
238
239 (ii) MOLECULE TYPE: cDNA
240
241
242 (ix) FEATURE:
243 (A) NAME/KEY: CDS
244 (B) LOCATION: 47..1663
245
246
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
248
249 CTAAC TTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAAT ATG ACC ACC 55
250 Met Thr Thr
251 1
252
253 CCA GGA AAA GAG AAC TTT CGC CTG AAA AGT TAC AAG AAC AAA TCT CTG 103
254 Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn Lys Ser Leu
255 5 10 15
256
257 AAT CCC GAT GAG ATG CGC AGG AGG AGG GAG GAA GAA GGA CTG CAG TTA 151
258 Asn Pro Asp Glu Met Arg Arg Arg Arg Glu Glu Glu Gly Leu Gln Leu

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/444,994*DATE: 11/21/95
TIME: 08:57:12*INPUT SET: S7400.raw*

| Line | Error | Original Text |
|------|--|---------------|
| 542 | Stop Codon at end of sequence removed - no error | |
| 929 | Stop Codon at end of sequence removed - no error | |
| 1376 | Stop Codon at end of sequence removed - no error | |

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(d).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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